

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5           (i) APPLICANT: Ashkenazi, Avi J.  
              Baker, Kevin  
              Chuntharapai, Anan  
              Gurney, Austin  
              Kim, Kyung Jin  
10           Wood, William

             (ii) TITLE OF INVENTION: Apo-2DcR

             (iii) NUMBER OF SEQUENCES: 13

15           (iv) CORRESPONDENCE ADDRESS:  
              (A) ADDRESSEE: Genentech, Inc.  
              (B) STREET: 1 DNA Way  
              (C) CITY: South San Francisco  
20           (D) STATE: California  
              (E) COUNTRY: USA  
              (F) ZIP: 94080

             (v) COMPUTER READABLE FORM:  
25           (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
              (B) COMPUTER: IBM PC compatible  
              (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
              (D) SOFTWARE: WinPatin (Genentech)

30           (vi) CURRENT APPLICATION DATA:  
              (A) APPLICATION NUMBER:  
              (B) FILING DATE: 12-Jun-1998  
              (C) CLASSIFICATION:

35           (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/049911

(B) FILING DATE: 18-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:

5

(A) NAME: Marschang, Diane L.

(B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1110P1

(ix) TELECOMMUNICATION INFORMATION:

10

(A) TELEPHONE: 650/225-5416

(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 259 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20

Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val  
1 5 10 15

25

Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg  
20 25 30

Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg  
35 40 45

30

His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser  
50 55 60

Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr  
65 70 75

35

	Thr	Asn	Ala	Ser	Asn	Asn	Glu	Pro	Ser	Cys	Phe	Pro	Cys	Thr	Val	
					80					85					90	
5	Cys	Lys	Ser	Asp	Gln	Lys	His	Lys	Ser	Ser	Cys	Thr	Met	Thr	Arg	
					95					100					105	
	Asp	Thr	Val	Cys	Gln	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	Glu	Asn	
					110					115					120	
10	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Ser	Arg	Cys	Pro	Ser	Gly	Glu	
					125					130					135	
	Val	Gln	Val	Ser	Asn	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	Cys	Val	
					140					145					150	
15	Glu	Glu	Phe	Gly	Ala	Asn	Ala	Thr	Val	Glu	Thr	Pro	Ala	Ala	Glu	
					155					160					165	
	Glu	Thr	Met	Asn	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	
20					170					175					180	
	Glu	Thr	Met	Asn	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	
					185					190					195	
25	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	
					200					205					210	
	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	
					215					220					225	
30	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Ser	His	Tyr	
					230					235					240	
	Leu	Ser	Cys	Thr	Ile	Val	Gly	Ile	Ile	Val	Leu	Ile	Val	Leu	Leu	
35					245					250					255	

Ile Val Phe Val  
259

(2) INFORMATION FOR SEQ ID NO:2:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15 GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50  
ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC 100  
CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC 150  
20 AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CC ATG 195  
Met  
1  
25 GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234  
Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile  
5 10  
30 GTC GCG GTC CTG CTG CCA GTC CTA GCT TAC TCT GCC ACC 273  
Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr  
15 20 25  
35 ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312  
Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala  
30 35 40

	CCA	CAG	CAA	CAG	AGG	CAC	AGC	TTC	AAG	GGG	GAG	GAG	TGT	351
	Pro	Gln	Gln	Gln	Arg	His	Ser	Phe	Lys	Gly	Glu	Glu	Cys	
					45					50				
5	CCA	GCA	GGA	TCT	CAT	AGA	TCA	GAA	CAT	ACT	GGA	GCC	TGT	390
	Pro	Ala	Gly	Ser	His	Arg	Ser	Glu	His	Thr	Gly	Ala	Cys	
		55				60					65			
10	AAC	CCG	TGC	ACA	GAG	GGT	GTG	GAT	TAC	ACC	AAC	GCT	TCC	429
	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Tyr	Thr	Asn	Ala	Ser	
				70				75						
15	AAC	AAT	GAA	CCT	TCT	TGC	TTC	CCA	TGT	ACA	GTT	TGT	AAA	468
	Asn	Asn	Glu	Pro	Ser	Cys	Phe	Pro	Cys	Thr	Val	Cys	Lys	
		80				85					90			
20	TCA	GAT	CAA	AAA	CAT	AAA	AGT	TCC	TGC	ACC	ATG	ACC	AGA	507
	Ser	Asp	Gln	Lys	His	Lys	Ser	Ser	Cys	Thr	Met	Thr	Arg	
			95				100					105		
25	GAC	ACA	GTG	TGT	CAG	TGT	AAA	GAA	GGC	ACC	TTC	CGG	AAT	546
	Asp	Thr	Val	Cys	Gln	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	
					110					115				
30	GAA	AAC	TCC	CCA	GAG	ATG	TGC	CGG	AAG	TGT	AGC	AGG	TGC	585
	Glu	Asn	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Ser	Arg	Cys	
		120					125					130		
35	CCT	AGT	GGG	GAA	GTC	CAA	GTC	AGT	AAT	TGT	ACG	TCC	TGG	624
	Pro	Ser	Gly	Glu	Val	Gln	Val	Ser	Asn	Cys	Thr	Ser	Trp	
				135				140						
40	GAT	GAT	ATC	CAG	TGT	GTT	GAA	GAA	TTT	GGT	GCC	AAT	GCC	663
	Asp	Asp	Ile	Gln	Cys	Val	Glu	Glu	Phe	Gly	Ala	Asn	Ala	
		145				150					155			

	ACT GTG GAA ACC CCA GCT GCT GAA GAG ACA ATG AAC ACC	702
	Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr	
	160 165 170	
5	AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG	741
	Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met	
	175 180	
10	AAC ACC AGC CCA GGG ACT CCT GCC CCA GCT GCT GAA GAG	780
	Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu	
	185 190 195	
15	ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT	819
	Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala	
	200 205	
20	GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA	858
	Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro	
	210 215 220	
25	GCT GCT GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT	897
	Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro	
	225 230 235	
30	GCC TCT TCT CAT TAC CTC TCA TGC ACC ATC GTA GGG ATC	936
	Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile	
	240 245	
35	ATA GTT CTA ATT GTG CTT CTG ATT GTG TTT GTT T	970
	Ile Val Leu Ile Val Leu Leu Ile Val Phe Val	
	250 255 259	
	GAAAGACTTC ACTGTGGAAG AAATTCCTTC CTTACCTGAA AGGTTTCAGGT	1020
35	AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC	1070

TCTGCTGTGT TCCCACAGAC AGAAACGCCT GCCCCTGCCC CAAAAAAAAA 1120

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1170

5 AAAAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15 Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly  
-40 -35 -30

20 Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro  
-25 -20 -15

Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro  
-10 -5 1 5

25 Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro  
10 15 20

Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro  
25 30 35

30 Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly  
40 45 50

Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala  
35 55 60 65

	Cys	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Tyr	Thr	Asn	Ala	Ser	Asn	
					70					75					80	
5	Asn	Glu	Pro	Ser	Cys	Phe	Pro	Cys	Thr	Val	Cys	Lys	Ser	Asp	Gln	
					85					90					95	
	Lys	His	Lys	Ser	Ser	Cys	Thr	Met	Thr	Arg	Asp	Thr	Val	Cys	Gln	
					100					105					110	
10	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	Glu	Asn	Ser	Pro	Glu	Met	Cys	
					115					120					125	
	Arg	Lys	Cys	Ser	Arg	Cys	Pro	Ser	Gly	Glu	Val	Gln	Val	Ser	Asn	
					130					135					140	
15	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	Cys	Val	Glu	Glu	Phe	Gly	Ala	
					145					150					155	
	Asn	Ala	Thr	Val	Glu	Thr	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	
20					160					165					170	
	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	
					175					180					185	
25	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	
					190					195					200	
	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	
					205					210					215	
30	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	
					220					225					230	
	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Ser	His	Tyr	Leu	Ser	Cys	Thr	Ile	
35					235					240					245	





	CTG CCA GTC CTA GCT TAC TCT GCC ACC ACT GCC CGG CAG	285
	Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln	
	20 25 30	
5	GAG GAA GTT CCC CAG CAG ACA GTG GCC CCA CAG CAA CAG	324
	Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln	
	35 40	
10	AGG CAC AGC TTC AAG GGG GAG GAG TGT CCA GCA GGA TCT	363
	Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser	
	45 50 55	
15	CAT AGA TCA GAA CAT ACT GGA GCC TGT AAC CCG TGC ACA	402
	His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr	
	60 65 70	
20	GAG GGT GTG GAT TAC ACC AAC GCT TCC AAC AAT GAA CCT	441
	Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro	
	75 80	
25	TCT TGC TTC CCA TGT ACA GTT TGT AAA TCA GAT CAA AAA	480
	Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys	
	85 90 95	
30	CAT AAA AGT TCC TGC ACC ATG ACC AGA GAC ACA GTG TGT	519
	His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys	
	100 105	
35	CAG TGT AAA GAA GGC ACC TTC CGG AAT GAA AAC TCC CCA	558
	Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro	
	110 115 120	
40	GAG ATG TGC CGG AAG TGT AGC AGG TGC CCT AGT GGG GAA	597
	Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu	
	125 130 135	

	GTC	CAA	GTC	AGT	AAT	TGT	ACG	TCC	TGG	GAT	GAT	ATC	CAG	636
	Val	Gln	Val	Ser	Asn	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	
					140					145				
5	TGT	GTT	GAA	GAA	TTT	GGT	GCC	AAT	GCC	ACT	GTG	GAA	ACC	675
	Cys	Val	Glu	Glu	Phe	Gly	Ala	Asn	Ala	Thr	Val	Glu	Thr	
		150					155					160		
	CCA	GCT	GCT	GAA	GAG	ACA	ATG	AAC	ACC	AGC	CCG	GGG	ACT	714
10	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	Ser	Pro	Gly	Thr	
				165					170					
	CCT	GCC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	AAC	ACC	AGC	CCA	753
	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	Ser	Pro	
15						175			180			185		
	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	ACC	ACC	792
	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	
			190					195				200		
20	AGC	CCG	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	831
	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	
					205					210				
25	ACC	ACC	AGC	CCG	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	870
	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	
		215					220					225		
	ACA	ATG	ACC	ACC	AGC	CCG	GGG	ACT	CCT	GCC	TCT	TCT	CAT	909
30	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Ser	His	
				230					235					
	TAC	CTC	TCA	TGC	ACC	ATC	GTA	GGG	ATC	ATA	GTT	CTA	ATT	948
	Tyr	Leu	Ser	Cys	Thr	Ile	Val	Gly	Ile	Ile	Val	Leu	Ile	
35		240					245				250			

GTG CTT CTG ATT GTG TTT GTT T GAAAGACTTC ACTGTGGAAG 990  
Val Leu Leu Ile Val Phe Val  
255 259

5 AAATTCCTTC CTTACCTGAA AGGTTTCAGGT AGGCGCTGGC TGAGGGCGGG 1040  
GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC 1090  
AGAAACGCCT GCCCCTGCCC CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140  
10 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:5:

15 (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 43 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTAAAACGA CGGCCAGTTA AATAGACCTG CAATTATTAA TCT 43

(2) INFORMATION FOR SEQ ID NO:6:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGGAAACAG CTATGACCAC CTGCACACCT GCAAATCCAT T 41

(2) INFORMATION FOR SEQ ID NO:7:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His  
1 5 10 15

15 Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly  
20 25 30

Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys  
35 40 45

20 Gly Cys Arg Lys  
49

25 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn  
1 5 10 15

35

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln  
20 25 30

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln  
5 35 40 45

Cys Lys Glu  
48

10 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1799 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

35

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCCACAA AATACACCGA CGATGCCCCG TCTACTTTAA GGGCTGAAAC 100

5 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145  
Met Glu  
1

10 CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184  
Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg  
5 10 15

15 AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223  
Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala  
20 25

20 AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262  
Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val  
30 35 40

25 GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301  
Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala  
45 50

CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340  
Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala  
55 60 65

30 GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379  
Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu  
70 75 80

TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418  
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp  
35 85 90

	TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC	457
	Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His	
	95 100 105	
5	TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT	496
	Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys	
	110 115	
10	GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC	535
	Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr	
	120 125 130	
15	AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG	574
	Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg	
	135 140 145	
20	GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA	613
	Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr	
	150 155	
25	GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA	652
	Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr	
	160 165 170	
30	CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC	691
	Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly	
	175 180	
35	ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT	730
	Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile	
	185 190 195	
40	GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA	769
	Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys	
	200 205 210	



	GTC	CTT	CCT	TAC	CTG	AAA	GGC	ATC	TGC	TCA	GGT	GGT	GGT	808
	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	
						215					220			
5	GGG	GAC	CCT	GAG	CGT	GTG	GAC	AGA	AGC	TCA	CAA	CGA	CCT	847
	Gly	Asp	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	
		225					230					235		
10	GGG	GCT	GAG	GAC	AAT	GTC	CTC	AAT	GAG	ATC	GTG	AGT	ATC	886
	Gly	Ala	Glu	Asp	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	
				240					245					
15	TTG	CAG	CCC	ACC	CAG	GTC	CCT	GAG	CAG	GAA	ATG	GAA	GTC	925
	Leu	Gln	Pro	Thr	Gln	Val	Pro	Glu	Gln	Glu	Met	Glu	Val	
	250					255					260			
20	CAG	GAG	CCA	GCA	GAG	CCA	ACA	GGT	GTC	AAC	ATG	TTG	TCC	964
	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	Val	Asn	Met	Leu	Ser	
			265					270					275	
25	CCC	GGG	GAG	TCA	GAG	CAT	CTG	CTG	GAA	CCG	GCA	GAA	GCT	1003
	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro	Ala	Glu	Ala	
					280					285				
30	GAA	AGG	TCT	CAG	AGG	AGG	AGG	CTG	CTG	GTT	CCA	GCA	AAT	1042
	Glu	Arg	Ser	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala	Asn	
		290					295					300		
35	GAA	GGT	GAT	CCC	ACT	GAG	ACT	CTG	AGA	CAG	TGC	TTC	GAT	1081
	Glu	Gly	Asp	Pro	Thr	Glu	Thr	Leu	Arg	Gln	Cys	Phe	Asp	
				305					310					
40	GAC	TTT	GCA	GAC	TTG	GTG	CCC	TTT	GAC	TCC	TGG	GAG	CCG	1120
	Asp	Phe	Ala	Asp	Leu	Val	Pro	Phe	Asp	Ser	Trp	Glu	Pro	
	315					320					325			

CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159  
 Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys  
 330 335 340

5 GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198  
 Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu  
 345 350

10 TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237  
 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg  
 355 360 365

15 GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276  
 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr  
 370 375

20 CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315  
 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His  
 380 385 390

25 TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354  
 Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn  
 395 400 405

30 GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400  
 Ala Asp Ser Ala Xaa Ser  
 410 411

CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450

35 AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC 1550

TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTT TGGGATGTCA 1650  
 TTGTTTTTAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700  
 5 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAG 1750  
 GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Glu	Gln	Arg	Gly	Gln	Asn	Ala	Pro	Ala	Ala	Ser	Gly	Ala	Arg	1	5	10	15
Lys	Arg	His	Gly	Pro	Gly	Pro	Arg	Glu	Ala	Arg	Gly	Ala	Arg	Pro	20	25	30	
Gly	Leu	Arg	Val	Pro	Lys	Thr	Leu	Val	Leu	Val	Val	Ala	Ala	Val	35	40	45	
Leu	Leu	Leu	Val	Ser	Ala	Glu	Ser	Ala	Leu	Ile	Thr	Gln	Gln	Asp	50	55	60	
Leu	Ala	Pro	Gln	Gln	Arg	Ala	Ala	Pro	Gln	Gln	Lys	Arg	Ser	Ser	65	70	75	
Pro	Ser	Glu	Gly	Leu	Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp	80	85	90	

	Gly	Arg	Asp	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr	
					95					100						105
5	His	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp	
					110					115						120
	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn	Thr	
					125					130						135
10	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	Glu	Glu	Asp	Ser	Pro	
					140					145						150
	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val	
					155					160						165
15	Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His	
					170					175						180
	Lys	Glu	Ser	Gly	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val	
20					185					190						195
	Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	
					200					205						210
25	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Asp	
					215					220						225
	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu	Asp	
					230					235						240
30	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln	Val	
					245					250						255
	Pro	Glu	Gln	Glu	Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	
35					260					265						270

Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro  
275 280 285

Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala  
290 295 300

Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp  
305 310 315

Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg  
320 325 330

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu  
335 340 345

Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp  
350 355 360

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp  
365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu  
380 385 390

Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn  
395 400 405

Ala Asp Ser Ala Xaa Ser  
410 411

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:13:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

20

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30